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(1) GENERAL INFORMATION:

- (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5141 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: TRISOMY 21 FETAL BRAIN cDNA LIBRARY
 - (B) CLONE: EHOC-1
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: 21q22.3
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 157..3729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGCAGGAAT CGGCACGAGG CGGCGCAACC GGCTCCGGAG CTGCCTGGCG CGGCCGGGCG	60
GGCGGCGCCG CTCAGGCTCG GGCTCCGGCT GGGCCCGGCG CGGCCTCGGG GCTGCCCATG	120
GGGCGCGGGG GGCCGGGCGG GTGACGCCGG ACGCCC ATG GAC GCC TCT GAG GAG	174
Met Asp Ala Ser Glu Glu	
1 5	
CCG CTG CCG CCG GTG ATC TAC ACC ATG GAG AAC AAG CCC ATC GTC ACC	222
Pro Leu Pro Pro Val Ile Tyr Thr Met Glu Asn Lys Pro Ile Val Thr	
10 15 20	
TGT GCT GGA GAT CAG AAT TTA TTT ACC TCT GTT TAT CCA ACG CTC TCT	270
Cys Ala Gly Asp Gln Asn Leu Phe Thr Ser Val Tyr Pro Thr Leu Ser	
25 30 35	
CAG CAG CTT CCA AGA GAA CCA ATG GAA TGG AGA AGG TCC TAT GGC CGG	318
Gln Gln Leu Pro Arg Glu Pro Met Glu Trp Arg Arg Ser Tyr Gly Arg	
40 45 50	
GCT CCG AAG ATG ATT CAC CTA GAG TCT AAC TTT GTT CAA TTC AAA GAG	366
Ala Pro Lys Met Ile His Leu Glu Ser Asn Phe Val Gln Phe Lys Glu	
55 60 65 70	
GAG CTG CTG CCC AAA GAA GGA AAC AAA GCT CTG CTC ACG TTT CCC TTC	414
Glu Leu Leu Pro Lys Glu Gly Asn Lys Ala Leu Leu Thr Phe Pro Phe	
75 80 85	
CTC CAT ATT TAC TGG ACA GAG TGC TGT GAT ACC GAA GTG TAT AAA GCT	462
Leu His Ile Tyr Trp Thr Glu Cys Cys Asp Thr Glu Val Tyr Lys Ala	
90 95 100	
ACA GTA AAA GAT GAC CTC ACC AAG TGG CAG AAT GTT CTG AAG GCT CAT	510
Thr Val Lys Asp Asp Leu Thr Lys Trp Gln Asn Val Leu Lys Ala His	
105 110 115	
AGC TCT GTG GAC TGG TTA ATA GTG ATA GTT GAA AAT GAT GCC AAG AAA	558
Ser Ser Val Asp Trp Leu Ile Val Ile Val Glu Asn Asp Ala Lys Lys	
120 125 130	
AAA AAC AAA ACC AAC ATC CTT CCC CGA ACC TCT ATT GTG GAC AAA ATA	606
Lys Asn Lys Thr Asn Ile Leu Pro Arg Thr Ser Ile Val Asp Lys Ile	
135 140 145 150	
AGA AAT GAT TTT TGT AAT AAA CAG AGT GAC AGG TGT GTT GTG CTC TCC	654
Arg Asn Asp Phe Cys Asn Lys Gln Ser Asp Arg Cys Val Val Leu Ser	
155 160 165	
GAC CCC TTG AAG GAC TCT TCT CGA ACT CAG GAA TCC TGG AAT GCC TTC	702
Asp Pro Leu Lys Asp Ser Ser Arg Thr Gln Glu Ser Trp Asn Ala Phe	
170 175 180	
CTG ACC AAA CTC AGG ACA TTG CTT CTT ATG TCT TTT ACC AAA AAC CTA	750
Leu Thr Lys Leu Arg Thr Leu Leu Met Ser Phe Thr Lys Asn Leu	
185 190 195	
GGC AAG TTT GAG GAT GAC ATG AGA ACC TTG AGG GAG AAG AGG ACT GAG	798
Gly Lys Phe Glu Asp Asp Met Arg Thr Leu Arg Glu Lys Arg Thr Glu	
200 205 210	
CCA GGC TGG AGC TTT TGT GAA TAT TTC ATG GTT CAG GAG GAG CTT GCC	846
Pro Gly Trp Ser Phe Cys Glu Tyr Phe Met Val Gln Glu Glu Leu Ala	
215 220 225 230	

0030307 = E. coli 660

TTT	GTT	TTC	GAG	ATG	CTG	CAG	CAG	TTC	GAG	GAC	GCC	CTG	GTG	CAG	TAC	894
Phe	Val	Phe	Glu	Met	Leu	Gln	Gln	Phe	Glu	Asp	Ala	Leu	Val	Gln	Tyr	
			235						240					245		
GAC	GAA	CTG	GAC	GCC	CTC	TTC	TCT	CAG	TAT	GTG	GTC	AAC	TTC	GGG	GCC	942
Asp	Glu	Leu	Asp	Ala	Leu	Phe	Ser	Gln	Tyr	Val	Val	Asn	Phe	Gly	Ala	
			250					255					260			
GGG	GAT	GGT	GCC	AAC	TGG	CTG	ACT	TTT	TTC	TGC	CAG	CCA	GTG	AAG	AGC	990
Gly	Asp	Gly	Ala	Asn	Trp	Leu	Thr	Phe	Phe	Cys	Gln	Pro	Val	Lys	Ser	
		265					270					275				
TGG	AAC	GGA	TTG	ATC	CTC	CGA	AAA	CCC	ATA	GAT	ATG	GAG	AAG	CGG	GAA	1038
Trp	Asn	Gly	Leu	Ile	Leu	Arg	Lys	Pro	Ile	Asp	Met	Glu	Lys	Arg	Glu	
	280					285					290					
TCG	ATC	CAG	AGG	CGA	GAA	GCC	ACC	CTG	TTA	GAT	CTG	CGC	AGT	TAC	CTG	1086
Ser	Ile	Gln	Arg	Arg	Glu	Ala	Thr	Leu	Leu	Asp	Leu	Arg	Ser	Tyr	Leu	
					300					305					310	
TTC	TCT	CGC	CAG	TGC	ACC	TTG	CTG	CTC	TTC	CTG	CAG	AGG	CCG	TGG	GAG	1134
Phe	Ser	Arg	Gln	Cys	Thr	Leu	Leu	Leu	Phe	Leu	Gln	Arg	Pro	Trp	Glu	
				315					320					325		
GTG	GCC	CAG	CGC	GCC	CTA	GAG	CTG	CTG	CAC	AAC	TGC	GTG	CAG	GAA	CTG	1182
Val	Ala	Gln	Arg	Ala	Leu	Glu	Leu	Leu	His	Asn	Cys	Val	Gln	Glu	Leu	
			330					335					340			
AAG	CTC	TTA	GAA	GTC	TCT	GTC	CCA	CCT	GGT	GCT	CTG	GAC	TGC	TGG	GTG	1230
Lys	Leu	Leu	Glu	Val	Ser	Val	Pro	Pro	Gly	Ala	Leu	Asp	Cys	Trp	Val	
			345				350					355				
TTT	CTG	AGC	TGT	CTG	GAG	GTG	TTG	CAG	AGG	ATA	GAA	GGC	TGC	TGT	GAC	1278
Phe	Leu	Ser	Cys	Leu	Glu	Val	Leu	Gln	Arg	Ile	Glu	Gly	Cys	Cys	Asp	
	360					365					370					
CGG	GCA	CAG	ATC	GAC	TCA	AAC	ATT	GCC	CAC	ACT	GTG	GGG	CTA	TGG	AGC	1326
Arg	Ala	Gln	Ile	Asp	Ser	Asn	Ile	Ala	His	Thr	Val	Gly	Leu	Trp	Ser	
	375				380				385						390	
TAT	GCC	ACA	GAA	AAG	TTA	AAG	TCC	TTG	GGC	TAT	CTA	TGT	GGA	CTT	GTG	1374
Tyr	Ala	Thr	Glu	Lys	Leu	Lys	Ser	Leu	Gly	Tyr	Leu	Cys	Gly	Leu	Val	
				395					400					405		
TCA	GAG	AAA	GGA	CCT	AAC	TCA	GAA	GAT	CTC	AAC	AGG	ACA	GTT	GAC	CTT	1422
Ser	Glu	Lys	Gly	Pro	Asn	Ser	Glu	Asp	Leu	Asn	Arg	Thr	Val	Asp	Leu	
			410					415					420			
TTG	GCA	GGT	TTG	GGA	GCT	GAG	CGA	CCA	GAA	ACA	GCC	AAC	ACA	GCT	CAG	1470
Leu	Ala	Gly	Leu	Gly	Ala	Glu	Arg	Pro	Glu	Thr	Ala	Asn	Thr	Ala	Gln	
		425					430					435				
AGT	CCT	TAT	AAG	AAA	CTG	AAA	GAA	GCA	TTA	TCG	TCA	GTG	GAA	GCT	TTT	1518
Ser	Pro	Tyr	Lys	Lys	Leu	Lys	Glu	Ala	Leu	Ser	Ser	Val	Glu	Ala	Phe	
	440					445					450					
GAA	AAA	CAC	TAC	TTA	GAT	TTG	TCC	CAT	GCC	ACC	ATT	GAA	ATG	TAT	ACA	1566
Glu	Lys	His	Tyr	Leu	Asp	Leu	Ser	His	Ala	Thr	Ile	Glu	Met	Tyr	Thr	
	455				460				465						470	
AGC	ATT	GGG	AGG	ATT	CGA	TCT	GCT	AAG	TTT	GTT	GGA	AAA	GAT	CTG	GCA	1614
Ser	Ile	Gly	Arg	Ile	Arg	Ser	Ala	Lys	Phe	Val	Gly	Lys	Asp	Leu	Ala	
				475					480					485		
GAG	TTT	TAC	ATG	AGG	AAA	AAG	GCT	CCA	CAA	AAG	GCA	GAA	ATC	TAT	CTT	1662
Glu	Phe	Tyr	Met	Arg	Lys	Lys	Ala	Pro	Gln	Lys	Ala	Glu	Ile	Tyr	Leu	
			490					495					500			

009001-226460

CAA Gln	GGA Gly	GCA Ala 505	CTG Leu	AAA Lys	AAC Asn	TAC Tyr	CTG Leu 510	GCT Ala	GAG Glu	GGC Gly	TGG Trp	GCA Ala 515	CTC Leu	CCC Pro	ATC Ile	1710
ACA Thr 520	CAC His	ACA Thr	AGG Arg	AAG Lys	CAG Gln	CTG Leu 525	GCC Ala	GAA Glu	TGT Cys	CAA Gln 530	AAG Lys	CAC His	CTT Leu	GGA Gly	CAA Gln	1758
ATT Ile 535	GAA Glu	AAC Asn	TAC Tyr	CTG Leu	CAG Gln 540	ACC Thr	AGC Ser	AGC Ser	CTC Leu	TTA Leu 545	GCC Ala	AGT Ser	GAC Asp	CAC His	CAC His 550	1806
CTC Leu	ACT Thr	GAA Glu	GAG Glu	GAG Glu 555	CGC Arg	AAG Lys	CAC His	TTC Phe	TGC Cys 560	CAG Gln	GAG Glu	ATA Ile	CTT Leu	GAC Asp 565	TTT Phe	1854
GCC Ala	AGC Ser	CAG Gln	CCG Pro 570	TCA Ser	GAC Asp	AGC Ser	CCA Pro	GGT Gly 575	CAT His	AAG Lys	ATA Ile	GTG Val	CTA Leu	CCC Pro	ATG Met	1902
CAT His	TCC Ser	TTT Phe 585	GCA Ala	CAA Gln	CTG Leu	CGA Arg	GAT Asp 590	CTC Leu	CAT His	TTT Phe	GAT Asp 595	CCC Pro	TCC Ser	AAT Asn	GCC Ala	1950
GTG Val 600	GTC Val	CAC His	GTG Val	GGC Gly	GGC Gly	GTT Val 605	TTG Leu	TGC Cys	GTT Val	GAG Glu	ATA Ile 610	ACC Thr	ATG Met	TAC Tyr	AGC Ser	1998
CAG Gln 615	ATG Met	CCT Pro	GTG Val	CCT Pro	GTT Val 620	CAC His	GTG Val	GAG Glu	CAG Gln	ATT Ile 625	GTG Val	GTC Val	AAT Asn	GTC Val	CAC His 630	2046
TTC Phe	AGC Ser	ATT Ile	GAG Glu	AAA Lys 635	AAC Asn	AGC Ser	TAC Tyr	CGG Arg	AAG Lys 640	ACT Thr	GCG Ala	GAG Glu	TGG Trp	CTT Leu 645	ACC Thr	2094
AAG Lys	CAC His	AAG Lys	ACG Thr 650	TCC Ser	AAT Asn	GGG Gly	ATC Ile	ATT Ile 655	AAC Asn	TTT Phe	CCA Pro	CCC Pro	GAG Glu 660	ACC Thr	GCA Ala	2142
CCT Pro	TTC Phe	CCT Pro 665	GTA Val	TCC Ser	CAA Gln	AAC Asn	AGT Ser 670	TTG Leu	CCC Pro	GCG Ala	CTG Leu	GAG Glu 675	TTG Leu	TAT Tyr	GAA Glu	2190
ATG Met 680	TTT Phe	GAG Glu	AGA Arg	AGC Ser	CCA Pro	TCT Ser 685	GAT Asp	AAC Asn	TCC Ser	TTG Leu 690	AAC Asn	ACG Thr	ACT Thr	GGG Gly	ATT Ile	2238
ATC Ile 695	TGC Cys	AGA Arg	AAC Asn	GTC Val	CAC His 700	ATG Met	CTC Leu	CTG Leu	AGA Arg	AGG Arg 705	CAG Gln	GAG Glu	AGC Ser	AGC Ser	TCC Ser 710	2286
TCT Ser	CTA Leu	GAG Glu	ATG Met	CCC Pro 715	TCA Ser	GGG Gly	GTG Val	GCT Ala	CTG Leu 720	GAG Glu	GAG Glu	GGT Gly	GCC Ala	CAC His 725	GTG Val	2334
CTG Leu	AGG Arg	TGC Cys	AGC Ser	CAC His 730	GTG Val	ACC Thr	CTG Leu	GAA Glu 735	CCA Pro	GGG Gly	GCC Ala	AAC Asn	CAG Gln 740	ATA Ile	ACA Thr	2382
TTC Phe	AGG Arg	ACT Thr 745	CAG Gln	GCC Ala	AAG Lys	GAA Glu	CCT Pro 750	GGA Gly	ACG Thr	TAT Tyr	ACA Thr	CTC Leu 755	AGG Arg	CAG Gln	CTG Leu	2430
TGC Cys 760	GCC Ala	TCG Ser	GTG Val	GGC Gly	TCC Ser	GTG Val 765	TGG Trp	TTC Phe	GTC Val	CTC Leu	CCT Pro 770	CAC His	ATC Ile	TAC Tyr	CCC Pro	2478

ATT Ile 775	GTG Val	CAG Gln	TAC Tyr	GAC Asp 780	GTG Val 780	TAC Tyr	TCA Ser	CAG Gln	GAG Glu	CCC Pro 785	CAG Gln	CTG Leu	CAC His	GTG Val	GAG Glu 790	2526
CCG Pro	CTG Leu	GCT Ala	GAT Asp 795	AGC Ser 795	CTT Leu	CTG Leu	GCA Ala	GGC Gly	ATT Ile 800	CCT Pro	CAG Gln	AGA Arg	GTC Val	AAG Lys 805	TTC Phe	2574
ACT Thr	GTC Val	ACT Thr	ACC Thr 810	GGC Gly	CAT His	GAT Asp	ACG Thr	ATA Ile 815	AAG Lys	AAT Asn	GGA Gly	GAC Asp 820	AGC Ser	CTG Leu	CAG Gln	2622
CTT Leu	AGC Ser	AAT Asn 825	GCC Ala	GAA Glu	GCC Ala	ATG Met	CTC Leu 830	ATC Ile	CTG Leu	TGC Cys	CAG Gln	GCG Ala 835	GAG Glu	AGC Ser	AGG Arg	2670
GCT Ala	GTG Val 840	GTC Val	TAC Tyr	TCC Ser	AAC Asn	ACG Thr 845	AGA Arg	GAA Glu	CAG Gln	TCT Ser	TCT Ser 850	GAG Glu	GCC Ala	GCG Ala	CTC Leu	2718
CGG Arg 855	ATT Ile	CAG Gln	TCC Ser	TCC Ser	GAC Asp 860	AAG Lys	GTC Val	ACG Thr	AGC Ser	ATC Ile 865	AGT Ser	CTG Leu	CCT Pro	GTT Val	GCG Ala 870	2766
CCT Pro	GCG Ala	TAC Tyr	CAC His	GTG Val 875	ATC Ile	GAA Glu	TTT Phe	GAA Glu	CTG Leu 880	GAA Glu	GTT Val	CTC Leu	TCT Ser	TTA Leu 885	CCT Pro	2814
TCA Ser	GCC Ala	CCA Pro	GCA Ala 890	CTC Leu	GGA Gly	GGG Gly	GAG Glu	AGT Ser 895	GAC Asp	ATG Met	CTG Leu	GGG Gly	ATG Met 900	GCA Ala	GAG Glu	2862
CCC Pro	CAC His	AGG Arg 905	AAG Lys	CAT His	AAG Lys	GAC Asp 910	AAA Lys	CAG Gln	AGA Arg	ACT Thr	GGC Gly	CGC Arg 915	TGC Cys	ATG Met	GTT Val	2910
ACC Thr	ACA Thr 920	GAC Asp	CAC His	AAA Lys	GTG Val	TCG Ser 925	ATT Ile	GAC Asp	TGC Cys	CCG Pro	TGG Trp 930	TCC Ser	ATC Ile	TAC Tyr	TCC Ser	2958
ACA Thr 935	GTC Val	ATC Ile	GCA Ala	CTG Leu	ACC Thr 940	TTC Phe	AGC Ser	GTA Val	CCC Pro	TTC Phe 945	AGG Arg	ACC Thr	ACA Thr	CAC His	AGC Ser 950	3006
CTC Leu	CTG Leu	TCC Ser	TCA Ser	GGA Gly 955	ACA Thr	CGG Arg	AAA Lys	TAT Tyr	GTT Val 960	CAA Gln	GTT Val	TGT Cys	GTC Val	CAG Gln 965	AAT Asn	3054
TTG Leu	TCA Ser	GAA Glu	CTT Leu 970	GAC Asp	TTT Phe	CAG Gln	CTG Leu	TCA Ser 975	GAT Asp	AGT Ser	TAT Tyr	CTT Leu	GTA Val 980	GAT Asp	ACC Thr	3102
GGT Gly	GAT Asp 985	AGT Ser	ACC Thr	GAC Asp	CTG Leu	CAA Gln	CTA Leu 990	GTA Val	CCA Pro	CTG Leu	AAC Asn	ACG Thr 995	CAG Gln	TCC Ser	CAG Gln	3150
CAG Gln	CCC Pro 1000	ATC Ile	TAC Tyr	AGC Ser	AAG Lys	CAG Gln 1005	TCG Ser	GTG Val	TTC Phe	TTC Phe	GTC Val 1010	TGG Trp	GAA Glu	CTC Leu	AAG Lys	3198
TGG Trp 1015	ACA Thr	GAA Glu	GAG Glu	CCT Pro	CCC Pro 1020	CCT Pro	TCT Ser	CTG Leu	CAT His	TGC Cys 1025	CGG Arg	TTC Phe	TCT Ser	GTT Val	GGA Gly 1030	3246
TTT Phe	TCC Ser	CCA Pro	GCT Ala	TCT Ser 1035	GAG Glu	GAA Glu	CAG Gln	CTG Leu	TCT Ser 1040	ATC Ile	TCC Ser	TTA Leu	AAG Lys	CCG Pro 1045	TAT Tyr	3294

ACT TAT GAA TTT AAA GTG GAA AAT TTT TTT ACA TTA TAC AAC GTG AAG 3342
 Thr Tyr Glu Phe Lys Val Glu Asn Phe Phe Thr Leu Tyr Asn Val Lys
 1050 1055 1060

GCT GAG ATC TTT CCC CCT TCG GGA ATG GAG TAT TGC AGA ACA GGC TCC 3390
 Ala Glu Ile Phe Pro Pro Ser Gly Met Glu Tyr Cys Arg Thr Gly Ser
 1065 1070 1075

CTC TGC TCC CTG GAG GTT TTG ATC ACG AGG CTC TCA GAC CTC TTG GAG 3438
 Leu Cys Ser Leu Glu Val Leu Ile Thr Arg Leu Ser Asp Leu Leu Glu
 1080 1085 1090

GTG GAT AAA GAT GAA GCA CTG ACT GAA TCT GAT GAG CAT TTT TCG ACA 3486
 Val Asp Lys Asp Glu Ala Leu Thr Glu Ser Asp Glu His Phe Ser Thr
 1095 1100 1105 1110

AAG CTT ATG TAT GAA GTT GTC GAC AAC AGT AGC AAC TGG GCA GTG TGT 3534
 Lys Leu Met Tyr Glu Val Val Asp Asn Ser Ser Asn Trp Ala Val Cys
 1115 1120 1125

GGG AAA AGC TGC GGT GTC ATC TCC ATG CCA GTG GCT GCT CGG GCC ACT 3582
 Gly Lys Ser Cys Gly Val Ile Ser Met Pro Val Ala Ala Arg Ala Thr
 1130 1135 1140

CAC AGG GTC CAC ATG GAA GTG ATG CCG CTC TTC GCC GGG TAT CTC CCC 3630
 His Arg Val His Met Glu Val Met Pro Leu Phe Ala Gly Tyr Leu Pro
 1145 1150 1155

CTG CCC GAC GTC AGG CTG TTC AAG TAC CTC CCC CAT CAT TCT GCA CAC 3678
 Leu Pro Asp Val Arg Leu Phe Lys Tyr Leu Pro His His Ser Ala His
 1160 1165 1170

TCC TCC CAA CTG GAC GCT GAC AGC TGG ATA GAA AAC GCA GCC TGT CAG 3726
 Ser Ser Gln Leu Asp Ala Asp Ser Trp Ile Glu Asn Ala Ala Cys Gln
 1175 1180 1185 1190

TAGACAAGCA CGGGGACGAC CAGCCGGACA GCAGCAGCCT CAAGAGCAGG GGCAGCGTGC 3786

ATTCGGCCTG CAGCAGCGAG CACAAAGGCC TACCCATGCC CCGGCTGCAG GCACTGCCGG 3846

CCGGCCAGGT CTTCAACTCC AGCTCGGGCA CACAAGTCCT GGTCATCCCC AGCCAAGATG 3906

ACCACGTCCT GGAAGTCAGT GTAACATGAC AACGCCAGGG TGAACACACG CCACTTCCCCA 3966

GCTAGGAGTG CACTTTATGG GACTGTGACT GGACTCTTCC GTTCTGGCTC CAGCCAGACC 4026

TTCAGTGGTC CTGCCTGGCC GTGGGGACAT CAGAGAGTGT CATCACGCAG CTGGCCAGCT 4086

GAGTTCTGTT GTTGTTTTCA TGCCGCCTGT GATCTCAGAT TCCTGCTTTT CTCACCCCGT 4146

CCCCATGCTG GTGTCCGACG CCGCTTACTC AGAGCCCTGG CCTCCCTCCC CCTACCTCAC 4206

ACGCTGCTCA TGAAAGTTTC CACCCACGCT GTCTCCACGG AACAGCCTCC GTCTGCTGGC 4266

TCTTCGTGGA AGGCCATTTG TCTTTCAGGT AGACACTCAG CAGCCCTCAC GGTCTTAGTG 4326

ACGTGTGTGC CTTTCTGGTC ACACAGCTGC CCAGTTTCCT GATCGGGGTG GATTTGTGTC 4386

CCCTAAGGGG TAAACAGCC GTTTACCGCA GATCCTCTCA TACACCCCTC TAGGGGAGGC 4446

GGGTGGGGGA GGGAGGGATC ATAACCCCTT CTGTGCCTTG GGATGCCGGA GCTGGGGGAC 4506

CTGGAGGCCC ATCAGCCGGA GCCACGTGAA AGGTACTGAA GAAAGCTGAG ACCCGGCTGT 4566

GAGGAGCGCC TCAGCGGTGA GGTGGTTTAG GGATAAATGT TTCTGGAACC CTGTGGTCCC 4626

CCATAATGTT GATAGATATC ATATGCACTG GGAGTTAAAT ATATTTAATT TAATGATCAT 4686

00322T E22H460

TATATATGTG GGGGTTAATA TGTTGTTTTT CTGTCCCTTT AAAGTCTTTA CATGTAATTG	4746
TAGCTGTATA ATCGTTATTT TTCTTTTGCA TCTTAAGTCT TAGAAATTAA GATATTCCAT	4806
CGTGAGGATG AGAGAGGTCC TCAGTGTGTT TTTGGTCTGG TTGTAGGGAA GGA CTCAAGT	4866
CCTGGAATGT CCTCCACTGG TCTACTGAGT TGCAGTCACA CTGTTCCAAT GGATTATTTG	4926
CTTTCGGTTG TAAATTTAAT TGTACATATG GTTGATTTAT TATTTTAAAA AATACAGACT	4986
AACTGATGTA ATGTTTATGT ATAAGTTGCA CCAAAAATCA AGGACAAAAA TAAGTGTGTT	5046
TGTTTTTACA GGTGTGAAAG TCACAGCTTG TAAATAAGTG TTGTATGTAT TAAACCTTTT	5106
CCAGTTCTCC AAAAAAAAAA AAAAAAAAAA AAAAA	5141

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1190 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Ala	Ser	Glu	Glu	Pro	Leu	Pro	Pro	Val	Ile	Tyr	Thr	Met	Glu
1				5					10					15	
Asn	Lys	Pro	Ile	Val	Thr	Cys	Ala	Gly	Asp	Gln	Asn	Leu	Phe	Thr	Ser
			20					25					30		
Val	Tyr	Pro	Thr	Leu	Ser	Gln	Gln	Leu	Pro	Arg	Glu	Pro	Met	Glu	Trp
			35				40					45			
Arg	Arg	Ser	Tyr	Gly	Arg	Ala	Pro	Lys	Met	Ile	His	Leu	Glu	Ser	Asn
	50					55					60				
Phe	Val	Gln	Phe	Lys	Glu	Glu	Leu	Leu	Pro	Lys	Glu	Gly	Asn	Lys	Ala
	65				70					75					80
Leu	Leu	Thr	Phe	Pro	Phe	Leu	His	Ile	Tyr	Trp	Thr	Glu	Cys	Cys	Asp
				85					90					95	
Thr	Glu	Val	Tyr	Lys	Ala	Thr	Val	Lys	Asp	Asp	Leu	Thr	Lys	Trp	Gln
			100					105					110		
Asn	Val	Leu	Lys	Ala	His	Ser	Ser	Val	Asp	Trp	Leu	Ile	Val	Ile	Val
		115					120					125			
Glu	Asn	Asp	Ala	Lys	Lys	Lys	Asn	Lys	Thr	Asn	Ile	Leu	Pro	Arg	Thr
	130					135					140				
Ser	Ile	Val	Asp	Lys	Ile	Arg	Asn	Asp	Phe	Cys	Asn	Lys	Gln	Ser	Asp
	145				150					155					160
Arg	Cys	Val	Val	Leu	Ser	Asp	Pro	Leu	Lys	Asp	Ser	Ser	Arg	Thr	Gln
				165					170					175	
Glu	Ser	Trp	Asn	Ala	Phe	Leu	Thr	Lys	Leu	Arg	Thr	Leu	Leu	Leu	Met
			180					185					190		
Ser	Phe	Thr	Lys	Asn	Leu	Gly	Lys	Phe	Glu	Asp	Asp	Met	Arg	Thr	Leu
			195				200					205			

Arg	Glu	Lys	Arg	Thr	Glu	Pro	Gly	Trp	Ser	Phe	Cys	Glu	Tyr	Phe	Met
210						215					220				
Val	Gln	Glu	Glu	Leu	Ala	Phe	Val	Phe	Glu	Met	Leu	Gln	Gln	Phe	Glu
225					230					235					240
Asp	Ala	Leu	Val	Gln	Tyr	Asp	Glu	Leu	Asp	Ala	Leu	Phe	Ser	Gln	Tyr
				245					250					255	
Val	Val	Asn	Phe	Gly	Ala	Gly	Asp	Gly	Ala	Asn	Trp	Leu	Thr	Phe	Phe
			260					265					270		
Cys	Gln	Pro	Val	Lys	Ser	Trp	Asn	Gly	Leu	Ile	Leu	Arg	Lys	Pro	Ile
		275					280					285			
Asp	Met	Glu	Lys	Arg	Glu	Ser	Ile	Gln	Arg	Arg	Glu	Ala	Thr	Leu	Leu
	290					295					300				
Asp	Leu	Arg	Ser	Tyr	Leu	Phe	Ser	Arg	Gln	Cys	Thr	Leu	Leu	Leu	Phe
305					310					315					320
Leu	Gln	Arg	Pro	Trp	Glu	Val	Ala	Gln	Arg	Ala	Leu	Glu	Leu	Leu	His
				325					330					335	
Asn	Cys	Val	Gln	Glu	Leu	Lys	Leu	Leu	Glu	Val	Ser	Val	Pro	Pro	Gly
			340					345					350		
Ala	Leu	Asp	Cys	Trp	Val	Phe	Leu	Ser	Cys	Leu	Glu	Val	Leu	Gln	Arg
		355					360					365			
Ile	Glu	Gly	Cys	Cys	Asp	Arg	Ala	Gln	Ile	Asp	Ser	Asn	Ile	Ala	His
	370					375					380				
Thr	Val	Gly	Leu	Trp	Ser	Tyr	Ala	Thr	Glu	Lys	Leu	Lys	Ser	Leu	Gly
385					390					395					400
Tyr	Leu	Cys	Gly	Leu	Val	Ser	Glu	Lys	Gly	Pro	Asn	Ser	Glu	Asp	Leu
				405					410					415	
Asn	Arg	Thr	Val	Asp	Leu	Leu	Ala	Gly	Leu	Gly	Ala	Glu	Arg	Pro	Glu
			420					425					430		
Thr	Ala	Asn	Thr	Ala	Gln	Ser	Pro	Tyr	Lys	Lys	Leu	Lys	Glu	Ala	Leu
		435					440					445			
Ser	Ser	Val	Glu	Ala	Phe	Glu	Lys	His	Tyr	Leu	Asp	Leu	Ser	His	Ala
		450				455					460				
Thr	Ile	Glu	Met	Tyr	Thr	Ser	Ile	Gly	Arg	Ile	Arg	Ser	Ala	Lys	Phe
465					470					475					480
Val	Gly	Lys	Asp	Leu	Ala	Glu	Phe	Tyr	Met	Arg	Lys	Lys	Ala	Pro	Gln
				485					490					495	
Lys	Ala	Glu	Ile	Tyr	Leu	Gln	Gly	Ala	Leu	Lys	Asn	Tyr	Leu	Ala	Glu
			500					505					510		
Gly	Trp	Ala	Leu	Pro	Ile	Thr	His	Thr	Arg	Lys	Gln	Leu	Ala	Glu	Cys
							520					525			
Gln	Lys	His	Leu	Gly	Gln	Ile	Glu	Asn	Tyr	Leu	Gln	Thr	Ser	Ser	Leu
						535					540				
Leu	Ala	Ser	Asp												

Gln Glu Ile Leu Asp Phe Ala Ser Gln Pro Ser Asp Ser Pro Gly His
 565 570 575
 Lys Ile Val Leu Pro Met His Ser Phe Ala Gln Leu Arg Asp Leu His
 580 585 590
 Phe Asp Pro Ser Asn Ala Val Val His Val Gly Gly Val Leu Cys Val
 595 600 605
 Glu Ile Thr Met Tyr Ser Gln Met Pro Val Pro Val His Val Glu Gln
 610 615 620
 Ile Val Val Asn Val His Phe Ser Ile Glu Lys Asn Ser Tyr Arg Lys
 625 630 635 640
 Thr Ala Glu Trp Leu Thr Lys His Lys Thr Ser Asn Gly Ile Ile Asn
 645 650 655
 Phe Pro Pro Glu Thr Ala Pro Phe Pro Val Ser Gln Asn Ser Leu Pro
 660 665 670
 Ala Leu Glu Leu Tyr Glu Met Phe Glu Arg Ser Pro Ser Asp Asn Ser
 675 680 685
 Leu Asn Thr Thr Gly Ile Ile Cys Arg Asn Val His Met Leu Leu Arg
 690 695 700
 Arg Gln Glu Ser Ser Ser Ser Leu Glu Met Pro Ser Gly Val Ala Leu
 705 710 715 720
 Glu Glu Gly Ala His Val Leu Arg Cys Ser His Val Thr Leu Glu Pro
 725 730 735
 Gly Ala Asn Gln Ile Thr Phe Arg Thr Gln Ala Lys Glu Pro Gly Thr
 740 745 750
 Tyr Thr Leu Arg Gln Leu Cys Ala Ser Val Gly Ser Val Trp Phe Val
 755 760 765
 Leu Pro His Ile Tyr Pro Ile Val Gln Tyr Asp Val Tyr Ser Gln Glu
 770 775 780
 Pro Gln Leu His Val Glu Pro Leu Ala Asp Ser Leu Leu Ala Gly Ile
 785 790 795 800
 Pro Gln Arg Val Lys Phe Thr Val Thr Thr Gly His Asp Thr Ile Lys
 805 810 815
 Asn Gly Asp Ser Leu Gln Leu Ser Asn Ala Glu Ala Met Leu Ile Leu
 820 825 830
 Cys Gln Ala Glu Ser Arg Ala Val Val Tyr Ser Asn Thr Arg Glu Gln
 835 840 845
 Ser Ser Glu Ala Ala Leu Arg Ile Gln Ser Ser Asp Lys Val Thr Ser
 850 855 860
 Ile Ser Leu Pro Val Ala Pro Ala Tyr His Val Ile Glu Phe Glu Leu
 865 870 875 880
 Glu Val Leu Ser Leu Pro Ser Ala Pro Ala Leu Gly Gly Glu Ser Asp
 885 890 895
 Met Leu Gly Met Ala Glu Pro His Arg Lys His Lys Asp Lys Gln Arg
 900 905 910

009227 " E.E. 644260

Thr Gly Arg Cys Met Val Thr Thr Asp His Lys Val Ser Ile Asp Cys
 915 920 925
 Pro Trp Ser Ile Tyr Ser Thr Val Ile Ala Leu Thr Phe Ser Val Pro
 930 935 940
 Phe Arg Thr Thr His Ser Leu Leu Ser Ser Gly Thr Arg Lys Tyr Val
 945 950 955 960
 Gln Val Cys Val Gln Asn Leu Ser Glu Leu Asp Phe Gln Leu Ser Asp
 965 970 975
 Ser Tyr Leu Val Asp Thr Gly Asp Ser Thr Asp Leu Gln Leu Val Pro
 980 985 990
 Leu Asn Thr Gln Ser Gln Gln Pro Ile Tyr Ser Lys Gln Ser Val Phe
 995 1000 1005
 Phe Val Trp Glu Leu Lys Trp Thr Glu Glu Pro Pro Pro Ser Leu His
 1010 1015 1020
 Cys Arg Phe Ser Val Gly Phe Ser Pro Ala Ser Glu Glu Gln Leu Ser
 1025 1030 1035 1040
 Ile Ser Leu Lys Pro Tyr Thr Tyr Glu Phe Lys Val Glu Asn Phe Phe
 1045 1050 1055
 Thr Leu Tyr Asn Val Lys Ala Glu Ile Phe Pro Pro Ser Gly Met Glu
 1060 1065 1070
 Tyr Cys Arg Thr Gly Ser Leu Cys Ser Leu Glu Val Leu Ile Thr Arg
 1075 1080 1085
 Leu Ser Asp Leu Leu Glu Val Asp Lys Asp Glu Ala Leu Thr Glu Ser
 1090 1095 1100
 Asp Glu His Phe Ser Thr Lys Leu Met Tyr Glu Val Val Asp Asn Ser
 1105 1110 1115 1120
 Ser Asn Trp Ala Val Cys Gly Lys Ser Cys Gly Val Ile Ser Met Pro
 1125 1130 1135
 Val Ala Ala Arg Ala Thr His Arg Val His Met Glu Val Met Pro Leu
 1140 1145 1150
 Phe Ala Gly Tyr Leu Pro Leu Pro Asp Val Arg Leu Phe Lys Tyr Leu
 1155 1160 1165
 Pro His His Ser Ala His Ser Ser Gln Leu Asp Ala Asp Ser Trp Ile
 1170 1175 1180
 Glu Asn Ala Ala Cys Gln
 1185 1190

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

004492 000000

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moraxella bovis*

(C) INDIVIDUAL ISOLATE: MboI linker

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTGATGCTC GAGTGAATTC

20

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